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The journal was published between 2013-2021 with the title of "Academic Platform - Journal of Engineering and Science". It will be published under its new title "Academic Platform Journal of Engineering and Smart Systems" after 2022.

Former Title: Academic Platform - Journal of Engineering and Science

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The Multicollinearity Effect on the Performance of Machine Learning Algorithms: Case Examples in Healthcare Modelling

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Abstract

The data extracted from various fields inherently consists of extremely correlated measurements in parallel with the exponential increase in the size of the data that need to be interpreted owing to the technological advances. This problem, called the multicollinearity, influences the performance of both statistical and machine learning algorithms. Statistical models proposed as a potential remedy to this problem have not been sufficiently evaluated in the literature. Therefore, a comprehensive comparison of statistical and machine learning models is required for addressing the multicollinearity problem. Statistical models (including Ridge, Liu, Lasso and Elastic Net regression) and the eight most important machine learning algorithms (including Cart, Knn, Mlp, MARS, Cubist, Svm, Bagging and XGBoost) are comprehensively compared by using two different healthcare datasets (including Body Fat and Cancer) having multicollinearity problem. The performance of the models is assessed through cross validation methods via root mean square error, mean absolute error and r-squared criteria. The results of the study revealed that statistical models outperformed machine learning models in terms of root mean square error, mean absolute error and r-squared criteria in both training and testing performance. Particularly the Liu regression often achieved better relative performance (up to 7.60% to 46.08% for Body Fat data set and up to 1.55% to 21.53% for Cancer data set on training performance and up to 1.56% to 38.08% for Body Fat data set and up to 3.50% to 23.29% for Cancer data set on testing performance) among regression methods as well as compared to machine algorithms. Liu regression is mostly disregarded in the machine learning literature, but since it outperforms the most powerful and widely used machine learning algorithms, it appears to be a promising tool in almost all fields, especially for regression-based studies including data with multicollinearity problem.

Keywords: Machine learning; Multicollinearity; Feature selection; Collinearity; Artificial intelligence

1. INTRODUCTION

Mathematical modeling mainly involves the processes of prediction and inference using a set of explanatory variables (i.e. attributes) that are considered to have an effect on a particular (i.e. target) variable. Facilitated by technological advances, the data collection process has significantly increased the scale of the variables. There have emerged highly correlated measurements that are assessed in almost every field, especially in areas such as health, marketing and finance [1]. In big databases containing thousands of variables, it is inevitable that complex patterns of relationships between variables will be discovered. The relationship is considered reasonable to a certain extent, but if it is extreme, a phenomenon known in the statistical literature as multicollinearity (i.e. collinearity) arises [2].

The multicollinearity problem stands out as a problem that is encountered quite frequently in the increasing data size with the ease of data collection in real life problems but is generally under-emphasized [3]. However, mathematically,

this problem causes both statistical and machine learning models to often yield inaccurate inferences and poor predictions (i.e. generalization ability).

The approaches to multicollinearity problem have differed in the statistics and machine learning literatures. In the statistics literature, the focus has been on variable selection by stepwise methods or theoretically modification of the classical ordinary least squares (OLS) estimator (like ridge, Liu estimator) by adding a penalty term to it [3]. In the field of machine learning, particularly in the field of artificial neural networks, models have been proposed with the assumption that they are not affected by multicollinearity due to the complex architecture [3, 4]. In the literature, the ridge estimator has received considerable attention in comparisons, while its alternative, the Liu estimator, has been relatively ignored. Therefore, there is a lack of a comprehensive comparison between machine learning methods and Liu regression.

In this study, we have compared the widely known models in the statistics literature (including Liu regression) with the most important machine learning models in the multicollinearity problem and aimed to contribute the following insights to the literature: (i) In addition to the widely known ridge, lasso and elastic net regression models, the Liu regression model is also considered in this study, (ii) it has been shown that statistical models can provide more effective results than complex machine learning models, (iii) the problem of multicollinearity has been demonstrated to be a problem that should not be ignored and can severely affect the performance of even the most powerful models.

The general layout of the study is as follows:

Section 2 presents the related studies on the subject. The problem of multicollinearity and possible diagnostic approaches are discussed in Section 3. The details about the models used in the study are explained in Section 4. The modelling process and experimental settings are covered in Section 5. The benchmarking results are reported in Section 6. A summary of the conclusions from the study is outlined in Section 7.

2. RELATED WORKS

In the context of multicollinearity, one of the first contributions in the statistical literature was made by James and Stein [5, 6], who proposed the Stein estimator based on equal shrinkage of the coefficients in the classical OLS model. Although this study is the foundation of shrinkage estimators, alternative estimators were required due to equal proportion shrinkage and the inability to handle coefficients with opposite sign. The most noteworthy contribution to this issue was presented by Hoerl and Kennard [7] by proposing the ridge estimator, which is based on shrinking towards zero instead of excluding correlated variables from the model by adding a penalty term to the classical OLS estimator. Since the choice of k in the Ridge estimator is quadratic and complex and that the Stein estimator shrinks all coefficients equally, there have been some disadvantages. Therefore, Liu [8] proposed the Liu estimator, which combines the Ridge and Stein estimator which is like Ridge but includes a penalty term in linear form as well as the Stein estimator properties. Stein, ridge and Liu estimators address the multicollinearity problem to a certain extent by shrinking the coefficients, but they do not have the ability to perform variable selection. The Least Absolute Shrinkage Selection Operator (Lasso), an alternative estimator that utilizes this capability, was proposed by Tibshirani [9]. The Lasso estimator can directly shrink variables to zero instead of shrinking them individually by keeping them in the model and thus making variable selection. To deal with the shortcomings of Lasso in the case of high dimensional and severe collinearity, Zou and Hastie [10] proposed a new estimator called elastic net, which is based on a process that incorporates both Ridge and Lasso simultaneously.

The studies in the field of machine learning have mainly developed within the framework of models based on artificial neural networks. Garg and Tai [4] proposed a model called FA-ANN based on factor analysis and artificial neural networks to deal with multicollinearity. Li and Niu [11]

introduced a new model called R-ELM for multicollinearity by incorporating ridge regression into the algorithm of an extreme learning machine which is a kind of a feed-forward neural network. Panduro and Torsen [12] suggested a two-stage model consisting of principal component analysis and stepwise regression models to overcome the problem of multicollinearity. Dumancas and Bello [13] compared correlated lipid profile data with twelve different machine learning methods (including ridge, lasso, elastic net, extreme gradient boosting, support vector machines etc.). Kilinc et al. [14] conducted a simulation study comparing genetic algorithm and multivariate adaptive splines models as variable selection methods in the presence of multicollinearity. A novel approach of feature selection based on the idea of feature filters has been carried out by Katrutsa and Strijov [15], enabling feature selection without regard to the prediction model. A CNN-based approach has been proposed by Hoseinzade and Haratizadeh [16] to model the correlation between various features in stock market data. Kim et al. [17] presented a combination of principal component analysis and artificial neural networks for correlated and high dimensional data. Obite et al. [18] have compared artificial neural networks and classical least squares models by using real and simulated datasets. Hua [19] proposed a approach of efficient data preprocessing with undersampling and embedded feature selection to address the imbalance of traffic samples and derive the leading features of incoming flows. Qaraad [20] introduced a hybrid optimization model for Cancer Classification to regularize and select the most informative subset of variables in a high-dimensional domain. Bi et al. [21] proposed a heterogeneous phoneme identification system including partial least squares and support vector machines to improve the diagnostic tasks for phoneme pronunciation for correlation data. Abubakar et al. [22] performed a simulation study and compared multiple regression, ridge regression, stepwise regression and partial least squares regression methods on a multicorrelated data. Mahadi et al. [23] introduced a new and efficient technique utilizing the recursive least squares (RLS) algorithms with a time-varying regularization parameter to ensure robustness and improve performance. Kaneko [24] presented a new criterion, called cross-validated permutation feature importance, to assess the feature importance ability of a machine learning model, particularly in the presence of multicollinearity issues. Genç [25] proposed a new regularized extreme learning machine (ELM) algorithm, square-root lasso ELM (SQRTL-ELM), to deal with the shortcomings of the extreme learning machine, including the instability, weak generalizability, and overfitting in the case of multicollinearity.

3. OVERVIEW OF THE MULTICOLLINEARITY

Multicollinearity refers to the near-linear dependencies among the explanatory (i.e. attribute) variables in a regression task. The reasons of this issue can be given as: (i) Data collection method, (ii) Constraints on model or population, (iii) Model identification errors and (iv) An over-defined model [26].

3.1. The Consequences of Multicollinearity

Multicollinearity can cause many serious problems, both theoretical and practical views [26, 27]. Montgomery et al. presented these problem as follows.

- i. The regression model yields coefficients with larger variances and covariances.
- ii. The absolute value of the coefficients can be obtained as larger.
- iii. Although there are exceptions, the model can often produce poorer predictions.

3.2. Multicollinearity Diagnostics

In the literature, various approaches have been proposed to detect the multicollinearity. These approaches are mainly based on the information of the data structure. This information is extracted by calculating the $X'X$ matrix which essentially represents the correlation matrix. The off-diagonal elements of $X'X$ matrix can provide us useful insights about the correlation level of explanatory variables. The common approaches based on this matrix are given as follows [26, 28]:

3.2.1. Calculation the Correlation Matrix

For a given X data matrix, the correlation matrix is obtained as follows:

$$r = X'X, \quad r_{ij} \neq 0 \quad (1)$$

where r_{ij} represents to the off-diagonal elements of the matrix. If r_{ij} exceeds a threshold (usually 0.70), this means that the corresponding variables have highly correlated each other. It may be insufficient to define multicollinearity due to treating variables as pair.

3.2.2. Variance Inflation Factor

Variance inflation factor (VIF) is based on the inverse of $X'X$ matrix. The off-diagonal elements of this inverse matrix provide a more useful and powerful information about the multicollinearity level and calculated as follows:

$$VIF_j = C_{ij} = (1 - R_j^2)^{-1} \quad (2)$$

where R_j^2 is the coefficient of determination calculated via the regression of x_j over the remain $p - 1$ variables. As the value of VIF depending on each variable increases, the severity of the multicollinearity increases. As a common practice, VIF values exceeding 5 or 10 provide strong evidence of a poor model in terms of generalization and estimation abilities [26].

3.2.3. Eigenvalues Analysis

The eigenvalues analysis is an alternative and beneficial approach to VIF or correlation-based approaches. It is mainly based on the decomposition the $X'X$ matrix into two-

different matrix including the eigenvalues and eigenvectors. This decomposition is defined as:

$$X'X = TAT' \quad (3)$$

where $A_{p \times p}$ is the diagonal matrix, whose diagonal elements correspond to the eigenvalues ($\lambda_i, i = 1, 2, \dots, p$) of $X'X$ matrix and $T_{p \times p}$ is the orthogonal matrix whose columns correspond to the eigenvectors of $X'X$ matrix. The presence of small-valued eigenvalues may be evidence of the existence of multicollinearity between the columns of the data. Instead of focusing each eigenvalue, condition number (CN) which is basically a representation of the spread of eigenvalues is commonly used and calculated as follows:

$$CN = \frac{\lambda_{max}}{\lambda_{min}} \quad (4)$$

where λ_{max} and λ_{min} correspond to the maximum and minimum eigenvalues obtained via TAT' eigen decomposition, respectively. For further details on this decomposition, please refer to Strang [29].

As a common practice, where a CN exceeding 1000 provides evidence for the existence of a severe multicollinearity, $100 < CN < 1000$ shows strong multicollinearity among the columns (i.e. variables) of data matrix [26].

3.3. Solutions to Multicollinearity

Various methods have been proposed in the literature to deal with the multicollinearity. Although the first recommended approach is to collect additional data, this may not always be possible due to the economic reasons or being impossible. The second is to use alternative approaches (like ridge, liu, lasso and elastic net regression) that do not rely on the calculation of least squares. Third, it is to redefine the model by creating new or groups of variables depending on the multi-correlated variables [26]. Finally, various pre-processing methods including centering, scaling, normalization, and standardization are applied as more common approaches for multicollinearity or other problems (like outliers) in the field of machine learning. For this study, we will focus on alternative models (like ridge, liu, lasso and elastic net regression).

4. THE OVERVIEW OF MODELS

4.1. Regression Models

Regression analysis is one of the major areas in machine learning and has been widely used for different learning tasks in various disciplines due to some superior properties like simplicity, interpretability and easy integrability. In a classical linear regression model can be expressed in a matrix notation as

$$y = X\beta + \varepsilon, \quad i = 1, 2, \dots, n \quad (5)$$

where y is an $(n \times 1)$ vector of the response variable, X is an $(n \times p)$ matrix of explanatory variables, β is a $(p \times 1)$

vector of coefficients to be estimated and $\boldsymbol{\varepsilon}$ is a $(n \times 1)$ vector of random errors.

The $\hat{\boldsymbol{\beta}}$ via OLS estimator can be obtained by using simple algebra as

$$\hat{\boldsymbol{\beta}}_{OLS} = (\mathbf{X}^T \mathbf{X})^{-1} \mathbf{X}^T \mathbf{y} \quad (6)$$

The ridge estimator, which is the most well-known and used in machine learning and data-oriented studies as an alternative to the OLS estimator, is proposed by Hoerl and Kennard [7] is defined as follows:

$$\hat{\boldsymbol{\beta}}_R = (\mathbf{X}^T \mathbf{X} + k \mathbf{I}_p)^{-1} \mathbf{X}^T \mathbf{y} \quad , \quad k \geq 0 \quad (7)$$

where k is called as ridge tuning parameter and \mathbf{I}_p shows the identity matrix of dimension p . Ridge estimator deals with the multicollinearity problem by adding a small positive term (k) to the diagonal elements of $\mathbf{X}^T \mathbf{X}$ matrix. For a positive optimal k value, the ridge estimator may provide better results than ordinary least squares. In short, ridge estimator improves OLS in terms of prediction accuracy and stability of coefficients for a certain amount of increasing on the bias.

Liu estimator was proposed by Liu [8] as an alternative to the ridge-type estimator to deal with multicollinearity. Although the idea behind the Liu estimator is similar in terms of shrinking the estimated with a small constant (i.e. Liu tuning parameter), the form of Liu tuning parameter in Liu estimator has a linear form, unlike the non-linear form in ridge estimator. The result of this situation is to be able to calculate easier and faster the Liu tuning parameter than the ridge tuning parameter. Another advantage of the Liu estimator over the ridge estimator is to be able to select the appropriate tuning parameter. The general form of the Liu estimator is given as

$$\hat{\boldsymbol{\beta}}_{Liu}^{(d)} = (\mathbf{X}^T \mathbf{X} + \mathbf{I}_p)^{-1} (\mathbf{X}^T \mathbf{y} + d \hat{\boldsymbol{\beta}}) \quad , \quad 0 < d < 1 \quad (8)$$

where d refers to the Liu tuning parameter and $\hat{\boldsymbol{\beta}}$ is the OLS estimator.

The least absolute shrinkage and selection operator (Lasso) is proposed by Tibshirani [9] in order to obtain a more predictive and sparse solution than OLS and ridge by carrying out variable selection. Lasso estimator is defined as

$$\hat{\boldsymbol{\beta}}_{Lasso} = \arg \min_{\boldsymbol{\beta}} \sum_{i=1}^N (y_i - \beta_0 - \sum_{j=1}^p x_{ij} \beta_j)^2 \quad (9)$$

$$\text{subject to} \quad \sum_{j=1}^p |\beta_j| \leq t$$

where t corresponds to the bound on the sum of the absolute values of coefficients and corresponding the upper limit of maximum size for expanding.

$\hat{\boldsymbol{\beta}}_{Lasso}$ can be also written in Lagrangian form as:

$$\hat{\boldsymbol{\beta}}_{Lasso} = \arg \min_{\boldsymbol{\beta}} \sum_{i=1}^N (y_i - \beta_0 - \sum_{j=1}^p x_{ij} \beta_j)^2 + \lambda \sum_{j=1}^p |\beta_j| \quad (10)$$

where λ is the Lagrangian multiplier.

Zou and Hastie [10] proposed the elastic net as a regularization and variable selection method. In the elastic net, the superiorities of both ridge and Lasso methods have been used in a unified model. Thus, an effective variable selection process can be carried out by considering the grouping effect (the relationships between variables). The naive elastic net estimator proposed by Zou and Hastie [8] is defined on a standardized data set as follows:

$$\hat{\boldsymbol{\beta}}_{ENet} = \arg \min_{\boldsymbol{\beta}} \sum_{i=1}^N (y_i - \beta_0 - \sum_{j=1}^p x_{ij} \beta_j)^2 + \lambda_1 \sum_{j=1}^p |\beta_j| + \lambda_2 \sum_{j=1}^p \beta_j^2 \quad (11)$$

where λ_1 and λ_2 are the non-negative constants corresponding to the size of the L_1 norm of the coefficients and the size of L_2 norm of the coefficients, respectively. The solution can be written as a constrained form of the optimization problem as

$$\hat{\boldsymbol{\beta}}_{ENet} = \arg \min_{\boldsymbol{\beta}} \sum_{i=1}^N (y_i - \beta_0 - \sum_{j=1}^p x_{ij} \beta_j)^2 \quad (12)$$

$$\text{subject to} \quad [(1 - \alpha) \sum_{j=1}^p |\beta_j| + \alpha \sum_{j=1}^p \beta_j^2] \leq t$$

where $\alpha \in [0,1]$ and determines the closeness of the solution of the ridge or lasso estimators. For $\alpha = 1$, the solution is equivalent to the ridge solution, and with $\alpha = 0$, the solution is reduced to the lasso solution.

4.2. Machine Learning Models

The machine learning models evaluated in this study can be divided into three subgroups: (i) Tree-based (CART, Bagging, Random Forests, Extreme Gradient Boosting), (ii) Kernel-based (Support Vector Machines), (iii) Instance-based (KNN), (iv) Splines-based (Cubist, MARS) and (v) Neural Networks-Based (Multilayer Perceptron). This section presents the main characteristics of each of these algorithms.

4.3. K-Nearest Neighbor (KNN)

K-Nearest Neighbors [30, 31] regression is a popular non-parametric supervised machine learning approach used for predicting continuous target variable based on the similarity of data points in a feature (i.e. attributes) space. It is based on identifying the k nearest neighbors to a given point and averaging the values of these neighbors to determine the prediction value of that point. This procedure can inherently be adapted easily to both classification and regression tasks. KNN regression requires the selection of the distance metric and the hyperparameter k (number of neighbors) which are generally found via cross-validation techniques. The local neighborhood of data points in the feature space is considered by the algorithm in an effort to minimize prediction error.

4.4. Support Vector Machines (SVM)

Support Vector Machines [32, 33] regression is a robust and flexible machine learning technique and has a goal to discover a hyperplane that maximizes the distance between the data points and the regression line. It performs this maximization step with observations called support vectors,

which represent a very small subset of observations. SVM assumes a hyperplane as follows:

$$f(x) = \langle w, x \rangle + b \quad (13)$$

where $f(x)$ corresponds to the target, w for the weight vector determining the direction of the hyperplane, x for the feature vector and b is the bias term used for the location of the hyperplane. The objective function is defined as:

$$\min_{w,b,\epsilon} \frac{1}{2} \|w\|^2 + C \sum_{i=1}^n \epsilon_i \quad (14)$$

with subject to the constraints:

$$y_i - \langle w, x_i \rangle - b \leq \epsilon_i, \quad \epsilon_i \geq 0, \quad i = 1, \dots, n \quad (15)$$

The trade-off between maximizing the margin and minimizing the error is determined by the hyperparameter C . SVM also gives the capability to explore possible non-linear relationships by transforming the data into a higher dimensional space with various functions called kernel functions (linear, polynomial, radial basis etc.).

4.5. Classification and Regression Trees (CART)

The Classification and Regression Trees [34] algorithm is well-known and fundamental machine learning algorithm that is a member of the decision tree family. In the context of regression, CART builds a binary tree structure where each internal node indicates an evaluation based on a particular attribute and each leaf node provides a prediction for the target variable.

The objective of CART regression is to split the feature space in such a way that the resulting tree minimizes the sum of squared differences between the predicted and actual target values. This recursive partitioning procedure is carried out until predefined stopping requirements have been met, such as a maximum tree depth or a specified number of data points in each leaf node.

4.6. Bagging

Bootstrap aggregation [35], often known as bagging, is an ensemble learning technique that seeks to enhance the prediction performance and robustness of regression models by the combination of numerous base models. Using bootstrapped subsets of the original training data, a set of separate and independently trained regression models—often decision trees (i.e. CART) or linear regressors—is built in bagging regression. These subsets are generated through random sampling with replacement, allowing certain data points to be included more than once while leaving out others. The predictions of these basis models are then combined to provide the final prediction. Each base model is trained on one specific subset.

4.7. Random Forests (RF)

The concept of bagging is extended to decision trees by the efficient ensemble learning technique known as Random

Forests [36]. Random Forests employs a group of decision tree regressors in the context of regression to generate accurate predictions. Similar to Bagging, multiple decision trees are built independently on bootstrapped subsets of the training data. Different from the bagging, only a random subset of attributes is taken into consideration for splitting at each split node of a tree. The final regression prediction is calculated by averaging the predictions of all the individual and decorrelated trees.

The strength of random forests regression algorithm appears in its ability to combine the interpretability of decision trees with the predictive power of ensemble learning. Each decision tree in the ensemble discovers a certain amount of the patterns in the data, and the predictions from every single tree collectively generate a more precise and stable prediction for the target variable.

4.8. Extreme Gradient Boosting (XGBoost)

The XGBoost [37] is a fundamental and state-of-the-art machine learning algorithms which can be used for both regression and classification tasks. It builds an ensemble of decision trees in a sequential manner (referring to the boosting), with each new tree being built to address the errors of the previous trees. Gradient descent optimization is employed to minimize the specific loss function (such as mean squared error) in each tree.

In order to improve model performance and training effectiveness, XGBoost incorporates a variety of novel strategies, such as a regularized objective function weighted quantile sketching and optimal feature splitting. With the comprehensive flexibility, XGBoost allows over hyperparameters, practitioners can customize the model's performance to achieve more versatile, robust and scalable results.

4.9. Cubist

The Cubist [38-40] algorithm for regression is a cutting-edge and effective algorithm that does exceptionally in capturing complex non-linear relationships in data while providing interpretability models. It integrates components of rule-based modeling and regression trees to produce a hybrid ensemble of regression model. It utilizes an innovative approach through the development of several models (including linear regressions, decision trees or rule-based learners), each of which focuses on various aspects of the structure of the data. In this way, Cubist stands out as a practical tool due to its interpretability and accurate predictions.

4.10. The Multivariate Adaptive Regression Splines (MARS)

MARS [41] is based on generating the piecewise-linear models via the elements of linear regression and decision trees. By splitting the input space into pieces and fitting linear models within each piece, MARS models have the ability to capture non-linear relationships. The approach can adaptively build the complexity of the model according to the data by selecting appropriate features and generating

basis functions via a forward and backward stepwise procedure. These features enhance the algorithm's ability to deal with noisy outliers and outliers and to capture interactions between attributes.

4.11. Multilayer Perceptron (MLP)

The MLP [42] algorithm is an artificial neural network architecture extending the principles of feedforward neural networks to capture complex relationships between input features and target variable. Each layer is in capable of handling and modifying the input data, and it is constructed up of several interconnected layers of artificial neurons. In order to minimize the difference between the predicted and actual target values, the network learns the ability to adjust its internal parameters, such as weights and biases, during training.

5. EXPERIMENTEL PROCESS AND SETTINGS

5.1. Data Description

In the study, two different datasets (Body Fat and Cancer) are utilized for the model comparison. The Body Fat set

originally shared by Johnson [43] and downloaded a commonly used database [44] for machine learning studies. The data set includes thirteen anthropometric measurements as explanatory variables and body fat percentage as the response variable belong to 252 individuals. Cancer data was retrieved from a publicly available database [45] to estimate the percentage of mortality due to cancer based on ten different variables belonging to 3047 individuals.

The datasets are investigated for multicollinearity by using the diagnostic methods presented in Section 3 and results are given in Tables 1-2. According to the results of Body Fat data, it can be said that there is a problem of multicollinearity in the data due to the presence of variables (weight, abdomen and hip) below the tolerance value of 0.1 and above the VIF value of 5. In addition, the condition value (CN:527.95) corresponds to a strong level of multicollinearity. Likewise, a similar interpretation can be drawn for the Cancer data as the condition number is 1265.84 and the VIF values calculated for some variables (such as avgAnnCount, popEst2015, PercentMarried) is greater than 5. The correlation analysis results given in Figures 1-2 also support the findings that there are high relationships between the variables.

Table 1. The results of multi-collinearity diagnostics of the Body Fat data

Variables	Tolerance	VIF	Symbol	Eigenvalue	Condition Index	CN
Age	0.4444	2.2505	λ_1	0.0732	13.7779	527.9409
Weight	0.0298	33.5093	λ_2	0.0206	25.9354	
Height	0.5972	1.6746	λ_3	0.0038	60.3083	
Neck	0.2312	4.3245	λ_4	0.0031	66.8449	
Chest	0.1057	9.4609	λ_5	0.0026	73.0770	
Abdomen	0.0850	11.7671	λ_6	0.0020	82.5060	
Hip	0.0676	14.7965	λ_7	0.0016	93.7259	
Thigh	0.1286	7.7779	λ_8	0.0012	107.3558	
Knee	0.2168	4.6121	λ_9	0.0008	134.3121	
Ankle	0.5241	1.9080	λ_{10}	0.0006	148.5825	
Biceps	0.2763	3.6197	λ_{11}	0.0006	155.0220	
Forearm	0.4561	2.1925	λ_{12}	0.0005	172.3598	
Wrist	0.2961	3.3775	λ_{13}	0.0001	316.5741	

Table 2. The results of multi-collinearity diagnostics of the Cancer data

Variables	Tolerance	VIF	Symbol	Eigenvalue	Condition Index	CN
avgAnnCount	0.129	7.73	λ_1	1.6456	2.2701	1265.8461
incidenceRate	0.935	1.07	λ_2	0.4700	4.2478	
medianIncome	0.276	3.63	λ_3	0.1823	6.8209	
popEst2015	0.130	7.71	λ_4	0.0973	9.3374	
povertyPercent	0.208	4.81	λ_5	0.0623	11.6623	
MedianAge	0.993	1.01	λ_6	0.0262	17.9836	
AvgHouseholdSize	0.809	1.24	λ_7	0.0204	20.4101	
PercentMarried	0.161	6.20	λ_8	0.0124	26.1204	
PctMarriedHouseholds	0.186	5.39	λ_9	0.0022	61.5450	
BirthRate	0.944	1.06	λ_{10}	0.0013	81.0914	

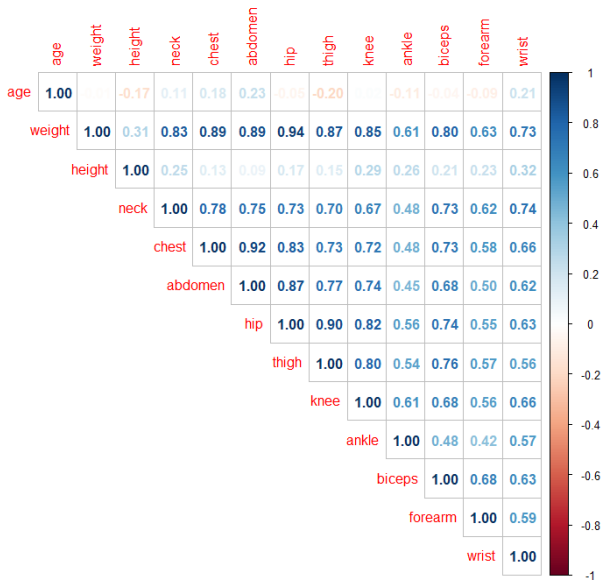


Figure 1. The correlation values between attributes for Body Fat data

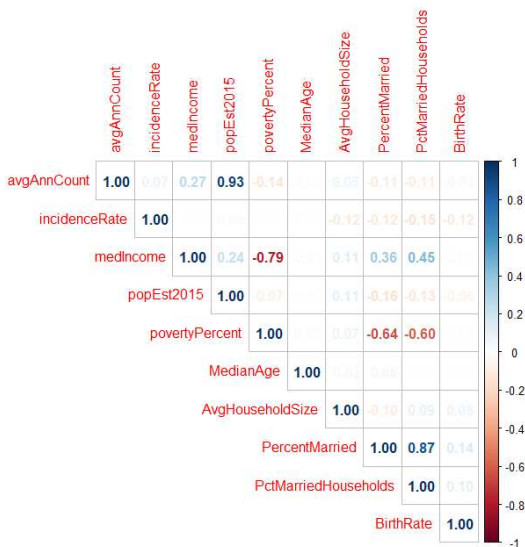


Figure 2. The correlation values between attributes for Cancer data

5.2. Performance Metrics

In regression studies of machine learning, the most common performance metrics can be given as (i) Root mean squared error, (ii) Mean absolute error and (iii) R square (the coefficient of determination). Each of this metric is calculated based on the difference between the target value (t_i) and the predicted value (y_i) by the model as follows:

$$RMSE = \sqrt{\frac{1}{n} \sum_{i=1}^n (t_i - y_i)^2} \tag{16}$$

$$MAE = \frac{1}{n} \sum_{i=1}^n |t_i - y_i| \tag{17}$$

$$R^2 = 1 - \frac{\sum_{i=1}^n (t_i - y_i)^2}{\sum_{i=1}^n (t_i - \bar{t})^2} \tag{18}$$

Among these metrics, while lower value of RMSE or MAE indicates a better model, higher values of R^2 provides a more explainable model. Due to the nature of the mathematical definition, the range of RMSE or MAE is $[0, \infty]$ and $[0, 1]$ for R^2 .

5.3. Preprocessing and Parameter Tuning

In the study, the data were preprocessed before performing an analysis. Initially, the data was centered to smooth out the high variability in the data structure. The data set is split into approximately seventy five percent as training data and twenty-five percent as test data. Statistical and machine learning models were built on the training data and the generalization performance was measured on the test data. During the training of the models, five-times ten-fold cross validation technique was used. The training performance of the models was calculated separately for each of the cross-validation data and the overall average was computed. A grid search space of twenty parameters was utilized to determine the model parameters. The details of parameters are given in Table 3. Each possible combination of parameters was trained by cross validating the models and the models with the best parameters were extracted. The performance (RMSE, MAE and R-Square values) of each model on the test data was calculated using the optimum parameter values.

Table 3. The ranges of parameters corresponding to each model

Model	Range of Parameters
CART	cost-complexity: [-10, -1] min_n: [2, 40]
Cubist	committees: [1, 100] neighbors: [0, 9]
Elastic Net	penalty: [-10, 0]
KNN	neighbors: [1, 15] dist_power: [0.1, 2]
Lasso	penalty: [-10, 0]
Liu	d: [0, 1]
MARS	prod_degree: [1, 2]
MLP	hidden_units: [1, 10] penalty: [-10, 0] epochs: [10, 1000]
RF	mtry: [1, 13] min_n: [2, 40]
Ridge	penalty: [-10, 0]
SVM (Poly)	cost: [-10, 5] degree: [1, 3]
SVM (Radial)	cost: [-10, 5] rbf_sigma: [-10, 0]
XGBoost	trees: [1, 2000] min_n: [2, 40] tree_depth: [1, 15] learn_rate: [-3, -0.5] loss_reduction: [-10, 1.5] sample_size: [0.1, 1]

Table 4. Performance comparisons of models corresponding to the train data set

Model	Data	RMSE	Mae	R ²
Bagging (CART)	Body Fat	4.672	3.956	0.683
	Cancer	8.176	6.144	0.458
CART	Body Fat	5.343	4.357	0.643
	Cancer	8.987	6.807	0.370
Cubist	Body Fat	4.525	3.795	0.763
	Cancer	8.095	6.118	0.468
Elastic Net	Body Fat	4.446	3.694	0.773
	Cancer	8.360	6.388	0.444
KNN	Body Fat	5.072	4.169	0.689
	Cancer	8.427	6.360	0.427
Lasso	Body Fat	4.451	3.677	0.773
	Cancer	8.374	6.409	0.431
Liu	Body Fat	4.111	3.398	0.818
	Cancer	7.825	6.007	0.512
MARS	Body Fat	4.423	3.506	0.715
	Cancer	8.138	6.093	0.463
MLP	Body Fat	6.005	4.814	0.500
	Cancer	9.971	7.634	0.182
RF	Body Fat	4.640	3.846	0.735
	Cancer	8.010	6.018	0.482
Ridge	Body Fat	4.668	3.756	0.686
	Cancer	8.373	6.413	0.431
SVM (Poly)	Body Fat	4.599	3.832	0.760
	Cancer	8.252	6.159	0.447
SVM (Radial)	Body Fat	4.668	3.664	0.699
	Cancer	8.467	6.458	0.429
XGBoost	Body Fat	4.736	3.901	0.725
	Cancer	7.949	5.966	0.488

Table 5. Performance comparisons of models corresponding to the testing data set

Model	Data	RMSE	Mae	R ²
Bagging (CART)	Body Fat	4.690	3.861	0.730
	Cancer	8.372	6.227	0.437
CART	Body Fat	5.855	4.942	0.547
	Cancer	9.037	6.892	0.363
Cubist	Body Fat	4.708	3.834	0.680
	Cancer	8.530	6.328	0.421
Elastic Net	Body Fat	4.530	3.569	0.701
	Cancer	9.000	6.668	0.364
KNN	Body Fat	5.071	4.251	0.634
	Cancer	8.611	6.501	0.406
Lasso	Body Fat	4.511	3.547	0.704
	Cancer	8.999	6.670	0.363
Liu	Body Fat	4.442	3.581	0.789
	Cancer	7.968	6.174	0.432
MARS	Body Fat	4.895	3.969	0.722
	Cancer	8.586	6.340	0.417
MLP	Body Fat	6.134	4.956	0.545
	Cancer	10.386	7.875	0.135
RF	Body Fat	4.6325	3.912	0.689
	Cancer	8.257	6.182	0.452
Ridge	Body Fat	4.689	3.816	0.750
	Cancer	8.971	6.664	0.363
SVM (Poly)	Body Fat	4.708	3.849	0.680
	Cancer	8.808	6.667	0.380
SVM (Radial)	Body Fat	4.782	3.939	0.725
	Cancer	9.160	6.513	0.342
XGBoost	Body Fat	4.9579	4.006	0.661
	Cancer	8.340	6.188	0.443

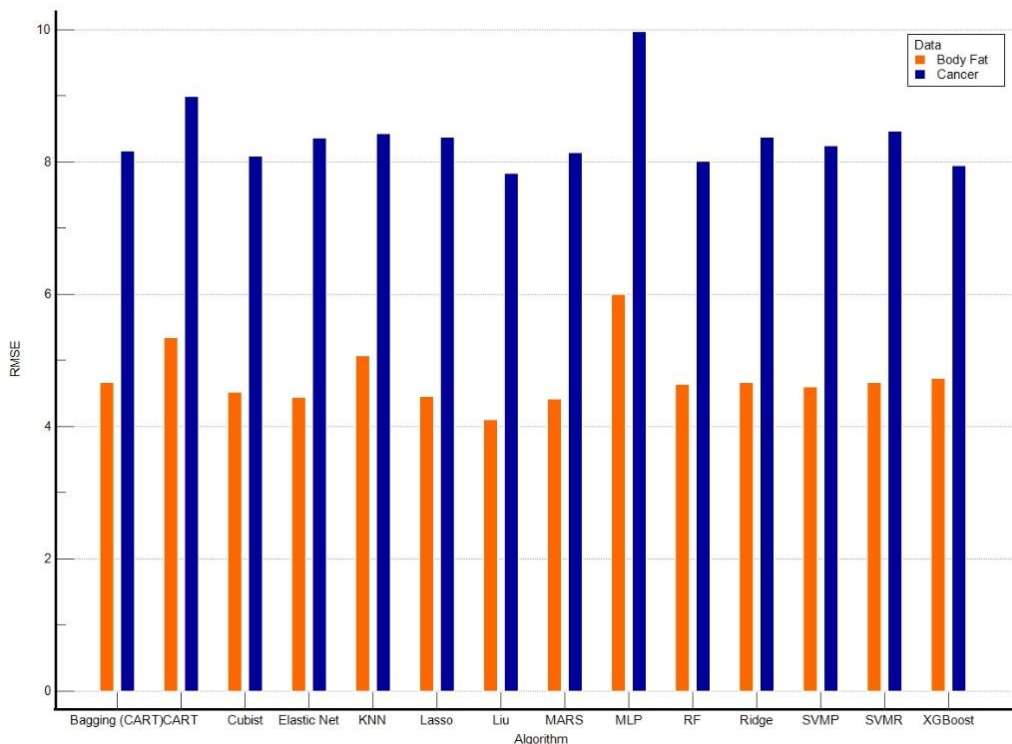


Figure 3. The visual representation of testing RMSE results for Body Fat and Cancer data sets

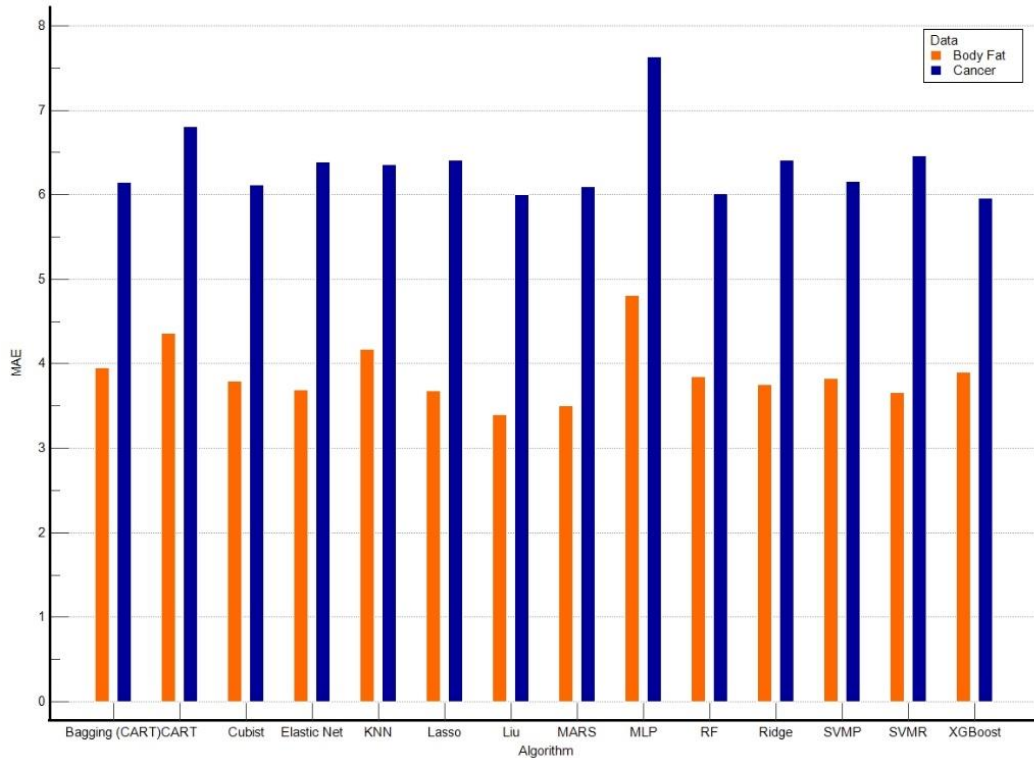


Figure 4. The visual representation of testing MAE results for Body Fat and Cancer data sets

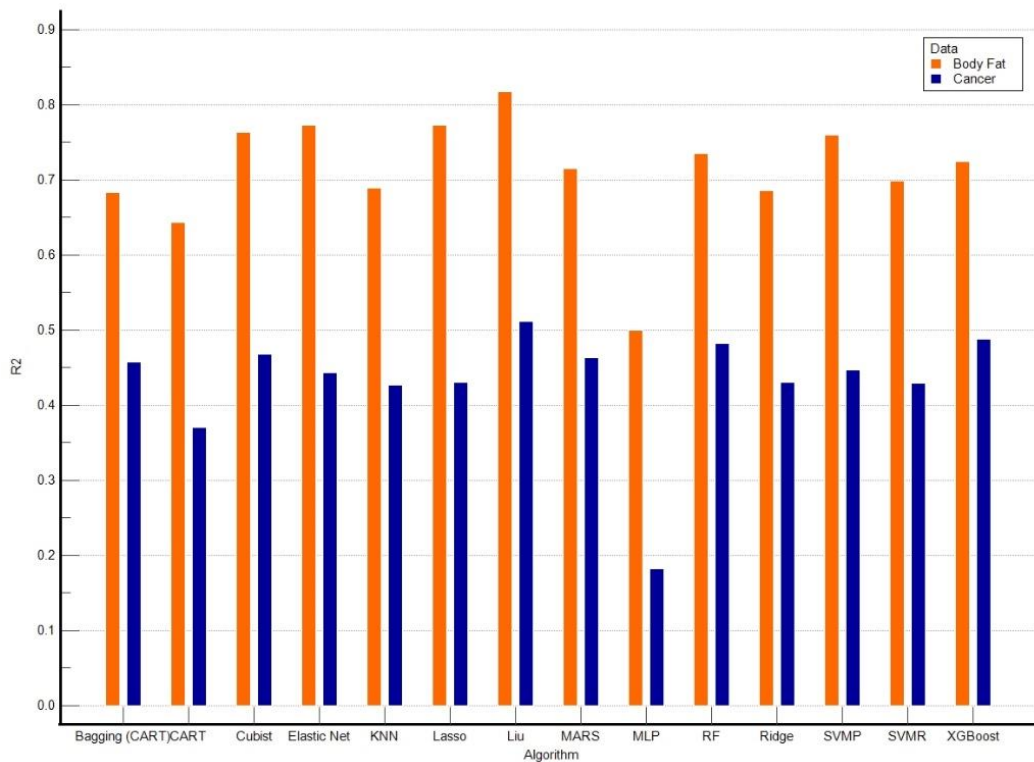


Figure 5. The visual representation of testing R-squared results for Body Fat and Cancer data sets

6. RESULTS

This section presents the results of thirteen different models including statistical and machine learning models. The comparison results of these models for two datasets are given in Table 4 for training data and Table 5 for test data. A visual representation of the performance values corresponding to the test data is given in Figures 3-5.

When the training performances of the models are evaluated for Body Fat data, the Liu regression model corresponding to the optimal parameter found as $d = 0.78$ (RMSE=4.111, MAE=3.398 and R-square=0.818) performed the best in each of the three performance criteria for this type of data set. In general, statistical models tend to perform better than machine learning models. The MLP, KNN and CART models showed the poorest performances, respectively.

Regarding the training performances for cancer data, Liu regression stands out in the RMSE (7.825) and R-square (0.512) criteria with $d = 0.86$ parameter value, while XGBoost is the best algorithm in the MAE (5.966) criterion. MLP and CART methods perform the weakest.

According to the test results, regression model was found to be the best model based on RMSE (4.442) and R-square (0.789) values, while Lasso regression model in the MAE (3.547) criterion. Liu, Lasso and Elastic Net regression models performed relatively close to each other but better than the remaining algorithms. Similar to the training performance, CART, KNN and MLP models showed weaker performance on the test data. Liu regression is superior to other algorithms in RMSE (7.968) and MAE (6.174) criteria in cancer data, whereas Random Forest algorithm has more generalizable performance with respect to R-square (0.452) value only. The SVM (with Radial kernel) and MLP algorithms were found to be the relatively weakest algorithms in the test performances.

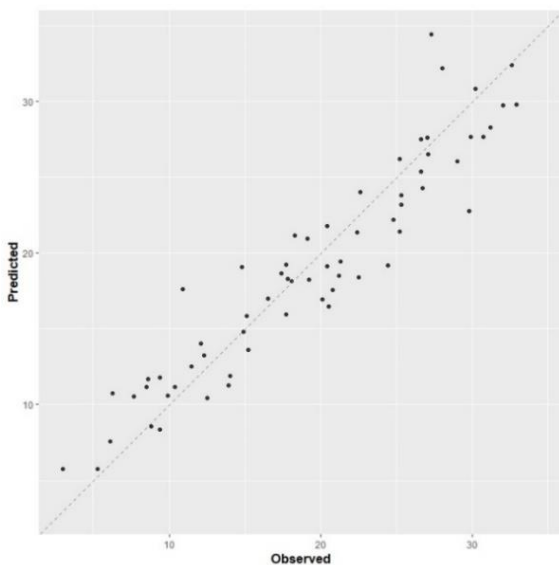


Figure 6. The scatter plot of observed and predicted value based on Liu regression testing results for Body Fat data

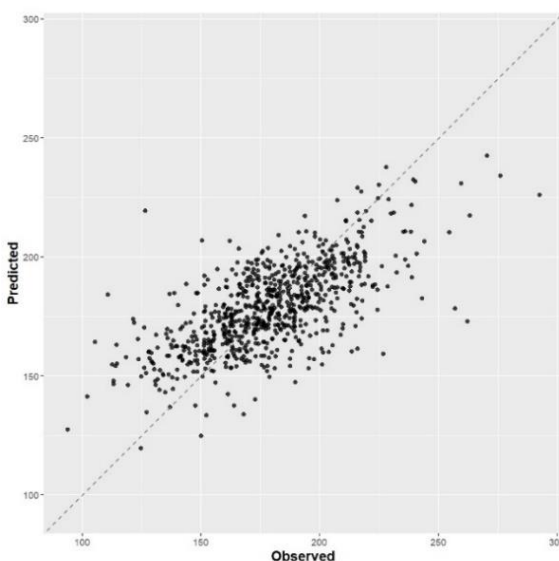


Figure 7. The scatter plot of observed and predicted value based on Liu regression testing results for Cancer data

The scatter plot generated to assess the fit between the predicted values of the Liu regression model and the actual response values is presented in Figure 6. According to this plot, it can be stated that the model predicts the actual response sufficiently well and provides values that are close to the actual values. The scatter plot provided in Figure 7 for cancer data confirms the similar interpretation and indicates that there is a strong fit between actual mortality rates and model predictions.

In the literature, it can be noted that the studies conducted on the body fat data are mainly along two directions: (i) Only statistics-oriented studies [46-47] and (ii) Studies based on a subset or different set of the data [48-51].

However, the results of the study reveal encouraging findings compared to the directly relevant studies in the literature. In the study conducted by Uçar et al. [52], our study produced better results compared to the comparison including artificial neural networks, support vector machines and decision trees algorithms (minimum RMSE=4.264 and R2=0.616). Additionally, the proposed approach is superior (RMSE=4.6384, MAE=3.6974) in comparison to the study carried out by Shao [53], applying multiple linear regression, artificial neural networks, MARS and support vector machines algorithms on the same data (RMSE=4.6384, MAE=3.6974).

The application of machine learning algorithms in cancer research is widespread, with a focus on cancer prognosis and prediction, incidence rates and survival prediction. Carrizosa et al. [54] developed a novel tree based linear regression model on the identical data, only focusing on hierarchical categorical variables. This study is not directly comparable as it does not incorporate different algorithms, but the prominent algorithm types are similar to some alternative studies [55-58]. However, it can be said that Liu regression is a promising and powerful alternative for future studies as it is one of the first examples of Liu regression in cancer studies as far as we know [59-60].

7. CONCLUSION AND FUTURE WORKS

In this study, the problem of multicollinearity is addressed, and comparative results of statistical and machine learning models based on two different healthcare datasets are presented. The models were trained using the cross-validation method and their generalization and prediction performances were assessed on an independent test data set.

The results of the study show that statistical models outperform for the data set suffering from multicollinearity problem, particularly Liu regression, complex machine learning models in both training and testing performance. However, the study encounters two key limitations. Firstly, it is critical that the degree of multicollinearity (weak, strong or extreme) is correctly identified and taken into account in the comparison process. Secondly, the tuning parameters (penalty parameters) of statistical methodologies have the potential to affect model performances by choosing them more accurately through analytical approaches rather than searching within a certain range. A more extensive study

taking into account these two limitations may yield valuable results in the forthcoming studies.

Consequently, the choice of the appropriate method is critical, given that the problem of multicollinearity is widespread in real-life applications. Therefore, it can be concluded that statistical models are powerful tools with effective solutions to the problem of multicollinearity.

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Using 3D U-Net for Brain Tumour Segmentation from Magnetic Resonance Images

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Abstract

Brain tumors within the skull can lead to serious health issues. The rapid and accurate detection and segmentation of tumor regions allow patients to receive appropriate treatment at an early stage, increasing their chances of recovery and survival. Various medical imaging methods, such as Magnetic Resonance Imaging (MRI), Positron Emission Tomography (PET), digital pathology, and Computed Tomography (CT), are used for the detection of brain tumors. Nowadays, with advancing technology and hardware, concepts like artificial intelligence (AI) and deep learning (DL) are becoming increasingly popular. Many AI methods are also being utilized in studies on brain tumor segmentation. This paper proposes a 3D U-Net DL model for brain tumor segmentation. The training and testing processes are carried out on the Brain Tumor Segmentation (BraTS) 2020 dataset, which is widely used in the literature. As a result, an Intersection over Union (IoU) score of 0.81, a Dice score of 0.87, and a pixel accuracy of 0.99 are achieved. The proposed model has the potential to assist experts in diagnosing the disease and developing appropriate treatment plans, thanks to its ability to segment brain tumors quickly and with high accuracy.

Keywords: Magnetic resonance images; Brain tumour; Deep learning; Semantic segmentation; 3D U-Net

1. INTRODUCTION

Cancer is the second most common cause of death in many countries, whether developed or underdeveloped [1]. Brain tumors are among the highest-risk types of cancer, especially in young patients [2]. Between 85% and 90% of primary central nervous system (CNS) cancers are of this kind. In 2020, it was projected that 308,102 individuals globally received a primary brain or spinal cord tumor diagnosis [3]. Early diagnosis and treatment of brain tumors greatly increase the chances of recovery.

Medical imaging is crucial for diagnosing diseases and planning their treatment. Nowadays, medical imaging equipment is rapidly developing, and a range of techniques like magnetic resonance imaging (MRI), computed tomography (CT), positron emission tomography (PET), and digital pathology are used. These techniques can provide incredibly detailed images of tissues and organs. In brain tumor patients, structures in the central nervous system and brain are generally examined using MRI, CT, and PET imaging technologies. However, evaluating and interpreting these images is a time-consuming and error-prone process.

Semantic segmentation is an image processing technique essential for the diagnosis and treatment of brain tumors.

This method assigns each pixel in brain images obtained through techniques such as MRI or CT to a specific class. For example, it can distinguish between different structures such as brain tissue, tumor lesions, and normal tissue [4]. In this way, the semantic segmentation method helps medical imaging experts quickly and accurately identify and classify brain tumors. This provides valuable information to healthcare professionals in important decision-making processes such as surgical planning, treatment management, and patient follow-up. It is also an important tool for early diagnosis and formulating personalized treatment strategies. Consequently, the significance of semantic segmentation in the realm of brain tumor diagnosis and treatment is garnering growing interest in both medical imaging research and applications [4].

In recent years, with the proliferation of deep learning (DL), there has been a surge of studies in the literature on brain tumor segmentation. In the study by Zhou et al., an efficient 3D residual neural network (ERV-Net) was proposed for brain tumor segmentation, featuring reduced computational complexity and lower GPU memory usage [5]. ERV-Net used 3D ShuffleNetV2, a computationally efficient network, primarily to reduce GPU memory usage and improve the efficiency of ERV-Net. The challenge of multimodal brain

tumor segmentation was tested on the BraTS 2018 dataset, achieving a Dice score of 91.21%.

The method developed in the study by Ye et al. represented a significant advancement in brain tumor segmentation through radiomic analysis [6]. Manual segmentation by radiologists is laborious and subjective, limiting the number of cases studied and hindering the reproducibility of clinical studies. In this context, a model incorporating a 3D Center-Cut Dense Block and a parallel network architecture was proposed for automatic tumor segmentation. This structure aimed to achieve detailed segmentation of medical images by decentralizing high-level control to lower layers of neural networks. Their architecture achieved notable success, obtaining an 88.4% Dice score and 83.8% sensitivity on the BraTS 2015 dataset, and an 88.7% Dice score and 84.3% sensitivity on the BraTS 2017 dataset.

The state-of-the-art model by Zhou et al. addressed challenges such as spatial information loss and inadequate multi-scale lesion processing faced by traditional deep convolutional neural networks in brain tumor segmentation [7]. This architecture enhanced the model's discrimination ability, particularly in segmenting tumors of varying sizes. Furthermore, the inclusion of a 3D fully connected Conditional Random Field enhanced results by incorporating both appearance and spatial consistency into the model's outputs. The model demonstrated consistent performance across different time periods and data conditions, achieving success rates of 86%, 82%, and 86% on the BraTS 2013, 2015, and 2018 datasets, respectively.

In the work by Zhang et al., Triple Intersecting U-Nets (TIU-Nets) were proposed for the segmentation of brain gliomas [8]. This model consists of two main components: the binary class segmentation U-Net (BU-Net) and the multi-class segmentation U-Net (MU-Net). The MU-Net utilizes multi-resolution features generated by the BU-Net. According to experimental results, the suggested 2D/3D TIU-Nets outperformed other cutting-edge techniques such as FCN, U-Net, SegNet, IVD-Net, FCDenseNet, DMFNet, CRDN, and DeepMedic in terms of segmentation accuracy. Additionally, the method achieved success rates of 82% on the BraTS 2015 dataset and 99.5% on the BrainWeb dataset. The proposed method improved segmentation accuracy and robustness by integrating advanced deep learning models [9]. Li et al. proposed a sophisticated approach for brain tumor segmentation that utilizes a combination of cascaded 3D U-Net and 3D U-Net++ architectures and got 89% Dice score.

Henry et al. proposed a 3D U-Net architecture enhanced with self-ensembling and deep supervision strategies to improve segmentation accuracy and robustness using the BraTS 2020 dataset. The model achieved a high Dice score of 90% [10]. In another study, the authors presented a novel approach to brain tumor segmentation using a 3D Generative Adversarial Network (GAN). The proposed method, called Vox2Vox, leverages the power of GANs to enhance the accuracy and robustness of segmentation in 3D medical images from the BraTS 2020 dataset. The model achieved Dice scores of 90% [11]. Lin et al. utilized a 3D U-Net architecture with deep supervision and context aggregation to enhance segmentation performance for the BraTS 2020 dataset and

obtained a Dice score of 92.3% [12]. Sasank and Venkateswarlu devised a novel approach to brain tumor segmentation that incorporates tumor growth prediction into the segmentation process [13]. The method aimed to enhance the accuracy of brain tumor segmentation by using a Full Resolution Convolutional Network (FrCN), which is capable of processing high-resolution images while maintaining spatial details. Based on experimental results, the method achieved accuracies of 97% for BraTS 2020, 95.56% for BraTS 2019, and 95.23% for BraTS 2018.

In this study, we aim to develop a fully automatic segmentation pipeline for MR images of brain tumors obtained from the BraTS 2020 dataset. To achieve this goal, we use the state-of-the-art 3D U-Net architecture. An experimental study is conducted on the proposed model, and its performance results are compared with those of other studies in the literature. The experimental results showed that the 3D U-Net achieved a pixel accuracy of 0.99, a Dice score of 0.87, and an IoU score of 0.81. In light of these results, this study provides evidence of suitable techniques for automatic brain tumor segmentation.

The rest of the paper is organized as follows: In the next section, an overview of the dataset and a formal definition of the segmentation algorithms are presented in detail. In the third section, the proposed architecture, performance metrics, and experimental results are discussed. Finally, section four concludes the paper.

2. MATERIALS AND METHODS

This section provides information about experimental dataset, background of segmentation and segmentation algorithms.

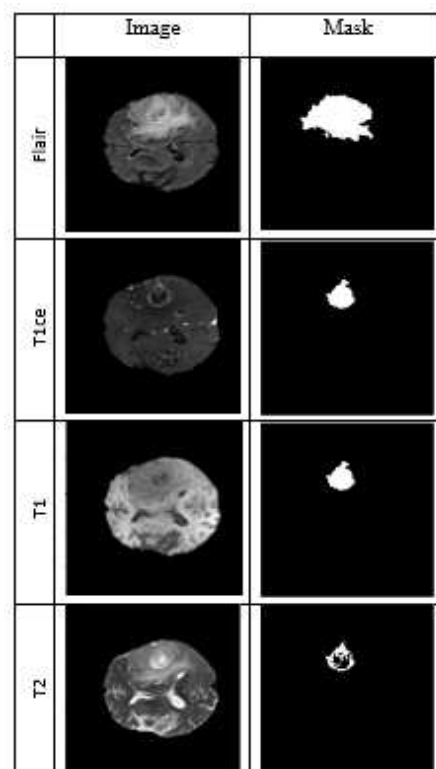


Figure 1. Samples from BraTS 2020 dataset

2.1. Dataset

The BraTS dataset, widely utilized in medical image segmentation studies, is the largest publicly available resource for brain tumor data [14]. Initially introduced in 2012 for the BraTS competition, the dataset has been regularly updated since. It consists of brain images captured using MRI devices, annotated and segmented by specialist doctors and radiologists. The dataset includes several versions, such as BraTS 2012, BraTS 2015, BraTS 2017, BraTS 2018, and BraTS 2020. Researchers have employed this dataset in various studies, including brain tumor detection, computer-aided diagnosis systems, and automatic medical image segmentation. In this study, the BraTS 2020 dataset obtained via the Kaggle platform is used [15].

The BraTS 2020 dataset used includes 369 MR images for training and 125 MR images for validation. Each brain image includes four distinct MRI modalities (FLAIR, T1ce, T1, T2) along with their corresponding masks, as illustrated in Figure 1.

These images in the dataset provide information about brain tissue. FLAIR images identify areas of edema, while T1ce images enhance the tumor boundary, revealing bright signals from substances accumulated in active cell areas [16]. T1 images depict healthy tissues, and T2 images are effective in highlighting bright signals indicating areas of edema. Each MRI modality consists of 155 slices, forming a 3D data structure for each brain when combined. This allows for a comprehensive examination and analysis of each modality and mask in 3D.

2.2. Segmentation

Image segmentation has been a fundamental problem in fields like computer vision and image processing for many years. This technique, used to understand and interpret images, involves dividing images into multiple segments and objects. Image segmentation plays a central role in various fields, including disease detection through medical images, tissue volume measurement, autonomous vehicles, video surveillance, and augmented reality [17].

Examining the network structure designs of medical image segmentation approaches reveals five main classes: Convolutional Neural Networks (CNNs), Autoencoder Networks (AEs), Fully Convolutional Networks (FCNs), Generative Adversarial Networks (GANs), and Region-Based Networks (R-FCNs) [4].

Our 3D U-Net model in this study is built on the U-Net architecture, placing it within the FCN class in terms of network structure.

2.2.1. Fully Convolutional Networks

FCNs are deep learning models commonly used for pixel-level classification tasks such as image segmentation. They are termed "Fully Convolutional" because each layer

includes convolution processes. These networks evolved from Convolutional Neural Network architectures [18]. Figure 2 illustrates the FCN architecture; unlike traditional CNNs, FCNs maintain the size of the input image at the output. In other words, the output size of FCNs matches the input size. To achieve this, up-sampling is performed on the output image [19].

FCNs are widely recognized in medical image segmentation studies for consistently improving and achieving successful results. The U-Net model, frequently employed in this field, represents an advanced form of the FCN model.

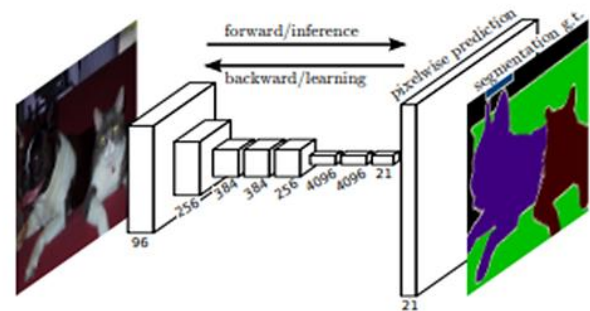


Figure 2. FCN architecture [19]

2.2.2. U-Net

The U-Net architecture, devised by Ronneberger et al. in 2015 for biomedical image segmentation, comprises 23 convolutional layers [20].

The model consists of two main components: the encoder and the decoder, as depicted in Figure 3. The encoder extracts features from medical images using convolutional layers, activation functions (ReLU), and pooling layers. Conversely, the decoder expands these features using upsampling layers. This expansion process enables precise localization of features within the image, thereby ensuring accurate and detailed segmentation [20].

2.2.3. 3D U-Net

This paper presents the 3D U-Net model, a powerful deep learning architecture created specifically for medical image segmentation [21]. Unlike traditional 2D convolutional neural networks, 3D U-Net processes data in three dimensions, making it particularly suitable for 3D medical imaging applications like MRI or CT scans. The model enhances the ability to identify complex structures in medical data by simultaneously capturing spatial features across height, width, and depth.

The encoder structure of the 3D U-Net model is composed of four blocks, similar to the original U-Net architecture. Each block includes convolution, dropout, and max-pooling 3D layers. In the decoder structure, each block begins with upsampling, followed by convolution and dropout layers. This ensures that the input brain MRI image is processed without altering its size at the output.

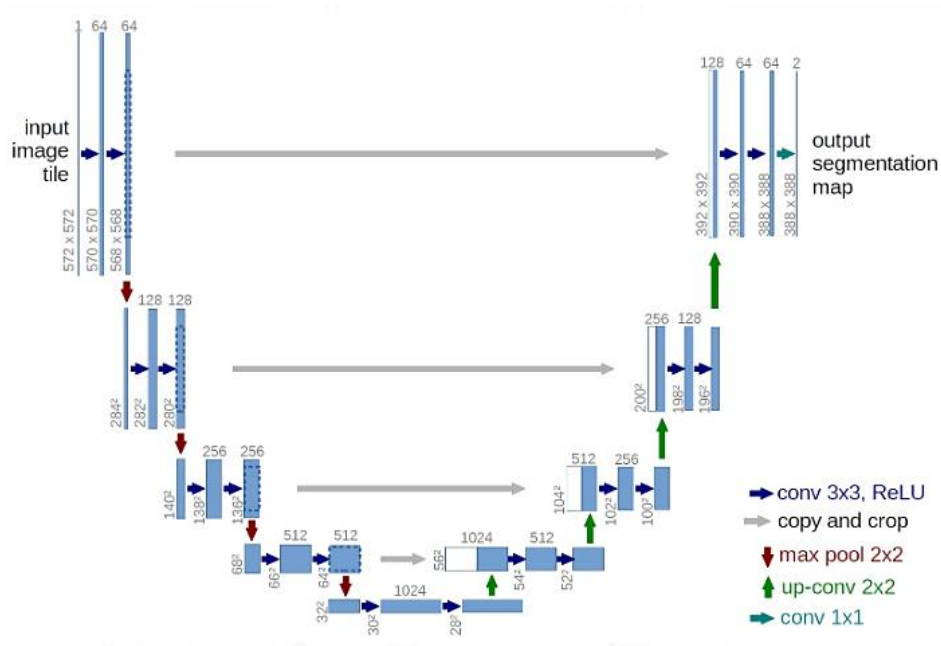


Figure 3. U-Net architecture [15]

3. EXPERIMENTAL STUDY

This section explains the proposed architecture with details. And evaluates the performance of 3D U-Net model via figures and tables.

3.1. Proposed Architecture

The proposed model comprises a total of 23 convolutional layers, as depicted in Figure 4. The encoder structure consists of four blocks. In the first block, the convolutional process utilizes 16 filters of size 3 x 3 x 3. The feature maps resulting from each convolutional process are then passed through the ReLU activation function. To reduce overfitting, a dropout layer with a rate of 0.1 is added, and a MaxPooling3D layer is applied to reduce the spatial dimensions by half.

The second block has a similar structure to the first block but uses 32 filters for the convolutional process. In the third and fourth blocks, 64 filters with a 0.2 dropout rate and 128 filters

with a 0.2 dropout rate are used, respectively. The sub-block, the deepest layer of the 3D U-Net architecture, utilizes 256 filters and a dropout ratio of 0.3. Max-pooling is not applied here because this block transitions to the decoder path.

In the decoder path, each block starts with upsampling, accomplished using the Conv3DTranspose layer. In the first upsampling block, convolution is performed with 128 filters and a dropout ratio of 0.2, and the feature maps from the corresponding block in the encoder path are concatenated. The second upsampling block follows a similar structure with 64 filters and a 0.2 dropout rate. The third and fourth upsampling blocks use 32 filters with a 0.1 dropout rate and 16 filters with a 0.1 dropout rate, respectively. Finally, a 1x1x1 convolutional process is applied for each class in the output layer, and the final segmentation output is produced using the softmax activation function. These stages enable the model to successfully learn fine details and complex structures in medical data, optimizing segmentation performance.

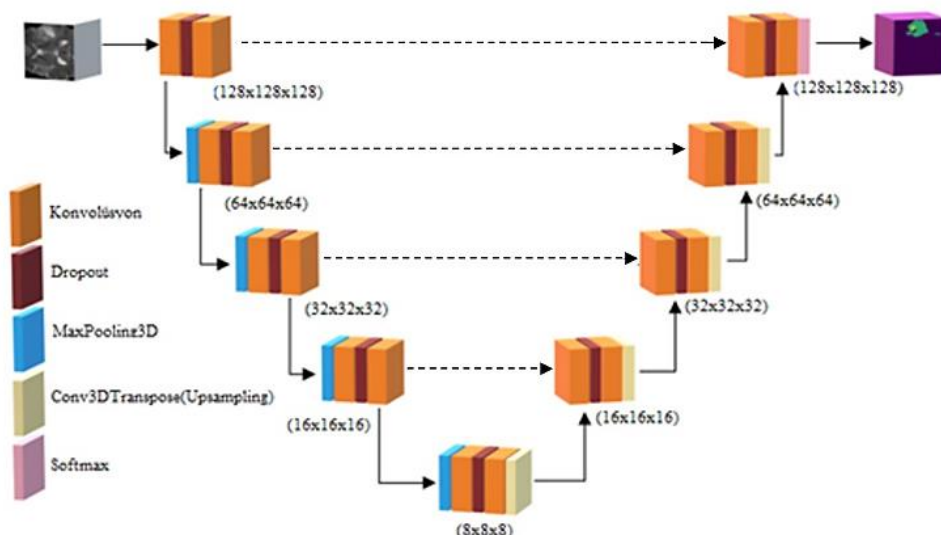


Figure 4. Proposed 3D U-Net architecture

3.2. Performance Metrics

The training and testing processes of the brain MRIs from the BraTS 2020 dataset were completed using the proposed 3D U-Net model. To evaluate the segmentation performance of the model, the commonly used metrics of Pixel Accuracy (1), Dice score (2), and IoU score (3) are employed based on the literature [16]. These metrics are calculated using True Positive (TP), False Positive (FP), True Negative (TN), and False Negative (FN).

TP represents the number of pixels or instances in both the ground truth and predicted segmentation that are accurately classified as part of the target class. FP is the number of pixels or instances that are incorrectly labelled as part of the target class in the segmentation prediction. TN refers to the pixels or instances that are correctly identified as not belonging to the target class in both the predicted segmentation and the ground truth segmentation. FN represents the number of pixels or instances in the ground truth that are part of the target class but were not recognized as such in the predicted segmentation.

Pixel accuracy refers to the ratio of correctly classified pixels to the total pixels in an image. This metric is often used in pixel-based classification problems such as image segmentation and is crucial for evaluating the overall performance of the model.

$$\text{Pixel Accuracy} = \frac{TP+TN}{TP+TN+FP+FN} \quad (1)$$

The Dice score is one of the most frequently used evaluation metrics in published medical image research.

$$\text{Dice Score} = \frac{2TP}{2TP+FP+FN} \quad (2)$$

The formula above measures the agreement between the predicted and ground truth segmentations, with a Dice score of 1 indicating perfect agreement and a score of 0 indicating no overlap.

The IoU score is a performance measure used in classification and segmentation problems, often employed in object detection and image segmentation. It measures how accurately a model's predictions match real objects. The IoU score is calculated using the following equation:

$$\text{IoU} = \frac{TP}{TP+FP+FN} \quad (3)$$

The IoU score calculates the ratio of the intersection area between the predicted objects and the real objects to their union area. It indicates the degree of overlap between the two regions representing the two clusters.

3.3. Experimental Results

The experimental research on the 3D U-Net model, developed for segmenting brain MRI images from the BraTS 2020 dataset, was conducted using the Python programming language. The model's training and testing were performed on a machine equipped with an Nvidia GeForce RTX 4060

GPU, utilizing Jupyter Notebook. TensorFlow and Keras libraries were employed for model development. During training, the batch size was optimized to 2, with 100 epochs and a learning rate set to 0.0001. The Adam optimizer was selected as the learning algorithm.

In the experiment, the pixel accuracy and loss values obtained during the training can be observed in Figures 4 and 5, respectively. Figure 4 illustrates that the proposed model achieved significant performance results in terms of pixel accuracy during both the training and validation stages.

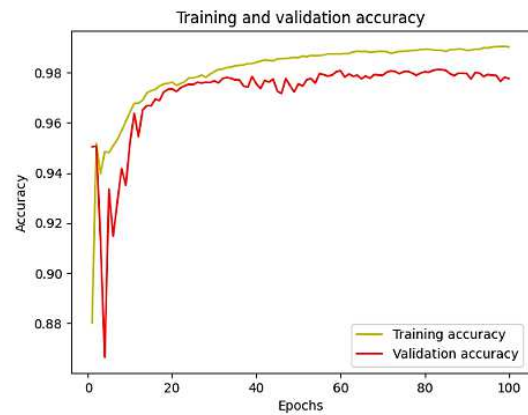


Figure 4. Train and validation set pixel accuracy

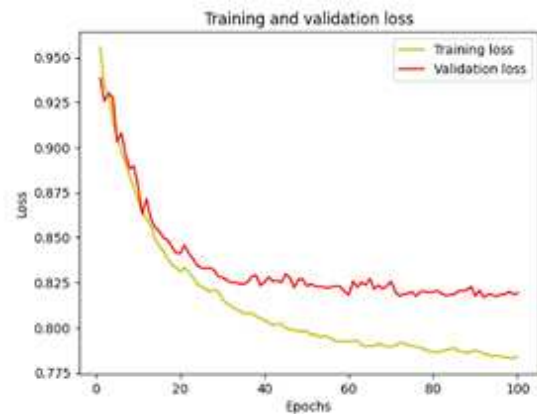


Figure 5. Train and validation set loss

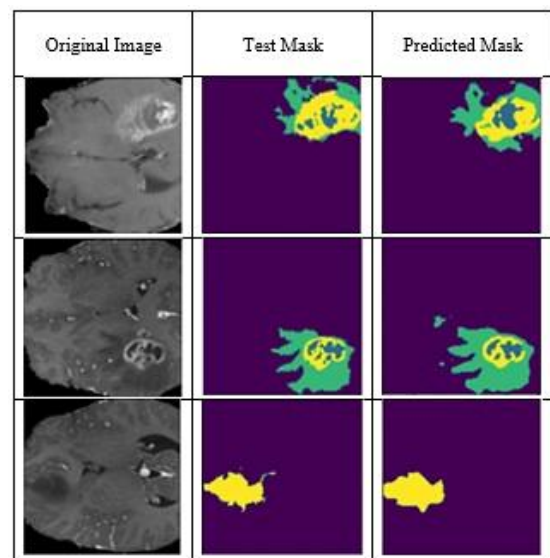


Figure 6. Visualized segmentation examples of MRI images

The test results of the proposed 3D U-Net model were evaluated using pixel accuracy, Dice score, and IoU score metrics. The model achieved a pixel accuracy of 0.99 during testing. The average Dice score and IoU score were 0.87 and 0.81, respectively.

Figure 6 displays visual results of the proposed model's brain tumour segmentation. The images illustrate the original brain MRI, the actual segmentation result, and the model's predicted segmentation output.

The model proposed in this study is compared with segmentation studies conducted on the BraTS datasets in Table 1, considering Dice score and pixel accuracy values from relevant studies. Reviewing the literature, it is evident that the proposed 3D U-Net model has achieved significant success.

Table 1. Comparing performances of studies using the BraTS dataset

Reference	Dataset	Pixel Accuracy	Dice Score
[4]	BraTS 2018	0.91	0.91
[5]	BraTS 2017	N/A	0.88
[6]	BraTS 2018	N/A	0.76
[7]	BraTS 2015	N/A	0.82
[10]	BraTS 2020	N/A	0.90
[11]	BraTS 2020	N/A	0.90
[12]	BraTS 2020	N/A	0.92
[13]	BraTS 2020	N/A	0.97
Proposed	BraTS 2020	0.99	0.87

4. CONCLUSION

A 3D U-Net segmentation model for the early diagnosis and detection of brain cancers was proposed in this study. The BraTS 2020 dataset was used to train and evaluate the suggested model. According to the experimental results, the model achieved an IoU score of 0.81, a Dice score of 0.87, and a pixel accuracy of 0.99.

Comparison with other studies in the literature demonstrated that the proposed model achieved significant performance results. It is anticipated that this model will be highly beneficial for radiologists, neurologists, and neurosurgeons working with brain MRI images, enabling rapid and accurate diagnoses. Therefore, the 3D U-Net segmentation model represents a promising approach for facilitating fast and accurate decision-making.

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